# Migratory connectivity analysis

**by EURING Migration Atlas**

*Charadrius hiaticula* **(EURING code 04700)**

## 1.1 Connectivity between individuals

The analysis evaluated 92 individuals (184 encounters) filtered from a total of 18536 records in the EURING databank which were considered for the Atlas. The species shows a significant connectivity from clustering, with a number of first-level clusters = 4 (Table 04700-1; Figure 04700-1).

**Table 04700-1.** Results from the migratory connectivity analysis. For each cluster, the degree of connectivity ($r_M$), its statistical significance (p-value) and 95% confidence interval limits are shown. When the p-value is less than or equal to 0.1, the degree of clustering structure (oasw) and the best number of clusters identified are reported.

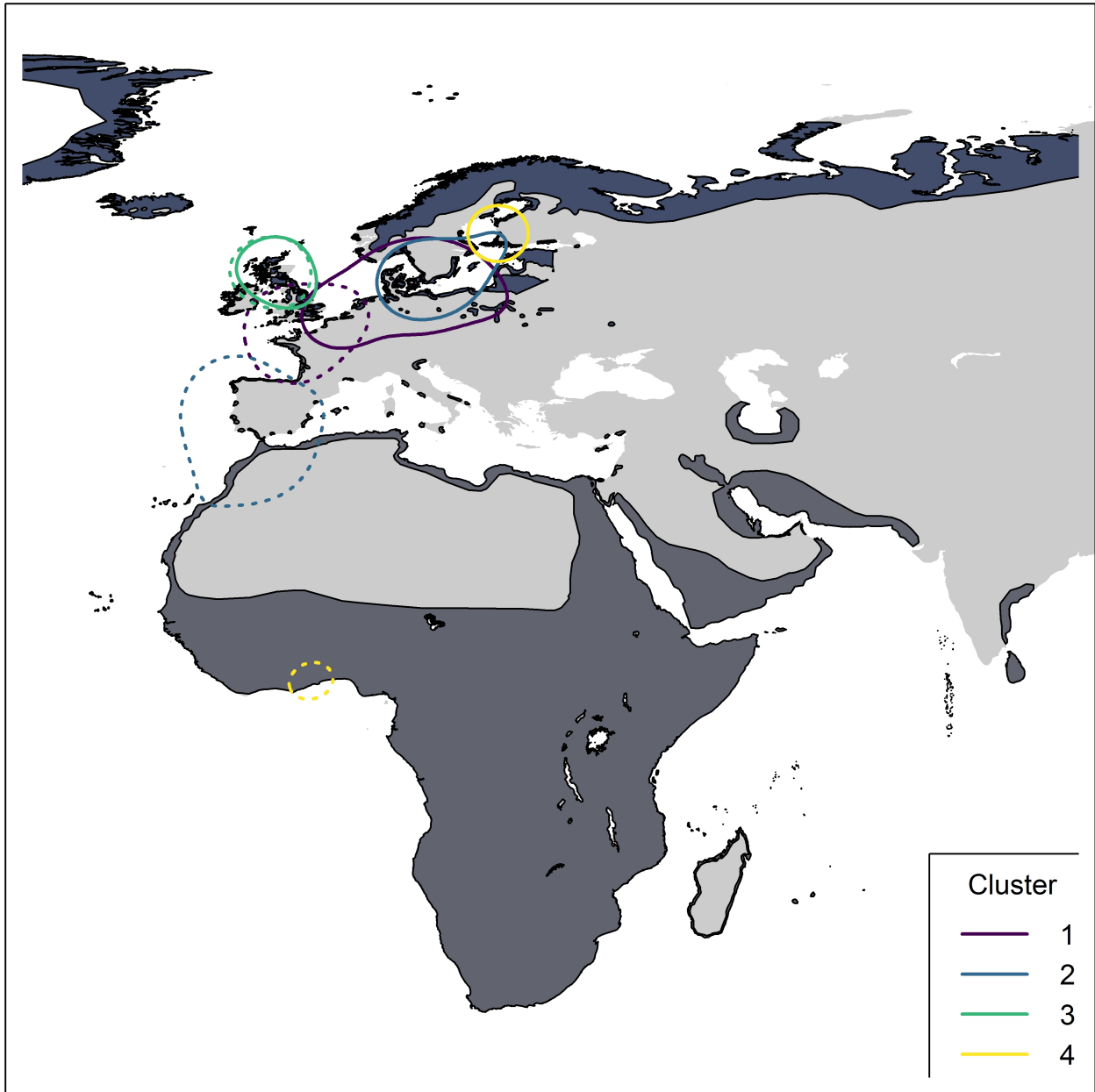| Cluster name | Level of clustering | N individuals | Migratory connectivity ($r_M$) | p-value | Lower 95% confidence limit | Upper 95% confidence limit | Best number of clusters | oasw |
|---|---|---|---|---|---|---|---|---|
| 0 | 0 | 92 | 0.447 | 0.001 | 0.289 | 0.619 | 4 | 0.522 |
| 1 | 1 | 42 | 0.021 | 0.342 | -0.073 | 0.285 | - | - |
| 2 | 1 | 26 | -0.056 | 0.573 | -0.136 | 0.288 | - | - |
| 3 | 1 | 21 | 0.545 | 0.001 | 0.307 | 0.908 | 5 | 0.512 |
| 4 | 1 | 3 | - | - | - | - | - | - |
| 31 | 2 | 8 | - | - | - | - | - | - |
| 32 | 2 | 4 | - | - | - | - | - | - |
| 33 | 2 | 5 | - | - | - | - | - | - |
| 34 | 2 | 2 | - | - | - | - | - | - |
| 35 | 2 | 2 | - | - | - | - | - | - |

**Figure 04700-1.** Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding range. Different contour colours correspond to different clusters, as reported in legend. The species distribution range is also shown (breeding range: blue; non-breeding range: dark grey; resident range: beige; from BirdLife International, 2019).

## 1.2 Sensitivity analysis

Results of power analysis and validation. Analyses at the species level were re-run on subsamples of individuals of decreasing size (100 repetitions per subsample size), according to simple random sampling of individuals (Figure 04700-2) and stratified sampling of individuals within the breeding range (Figure 04700-3) and the non breeding range (Figure 04700-4). For stratified sampling, we selected individuals with a

probability inversely proportional to the number of observation in each country. Figures below report the results of the procedure.
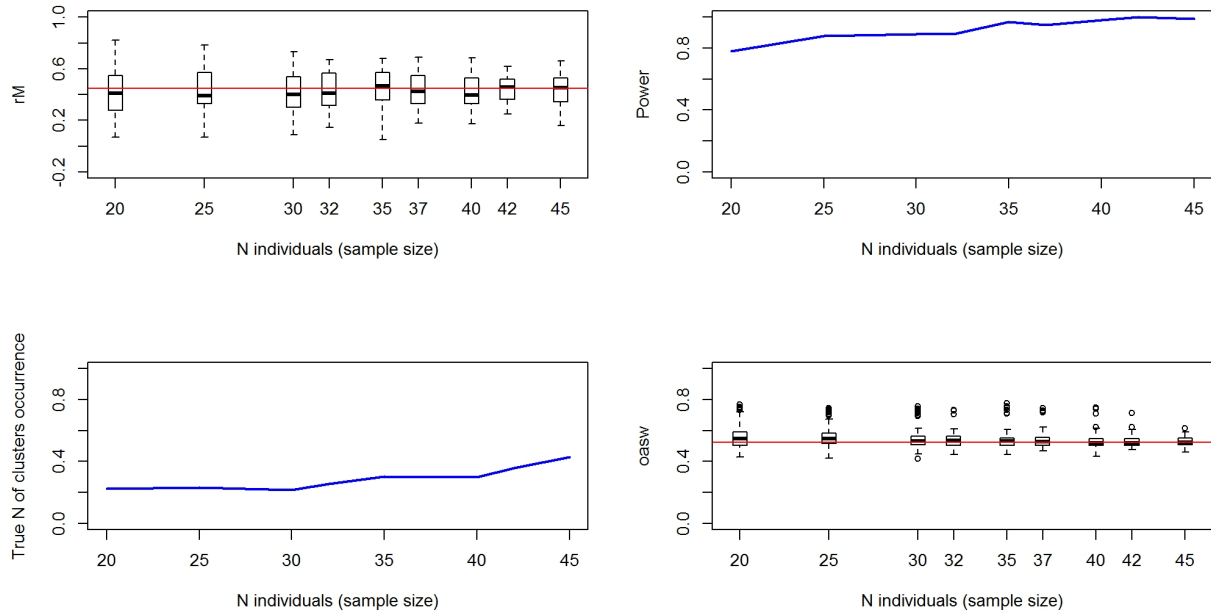


**Figure 04700-2.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.
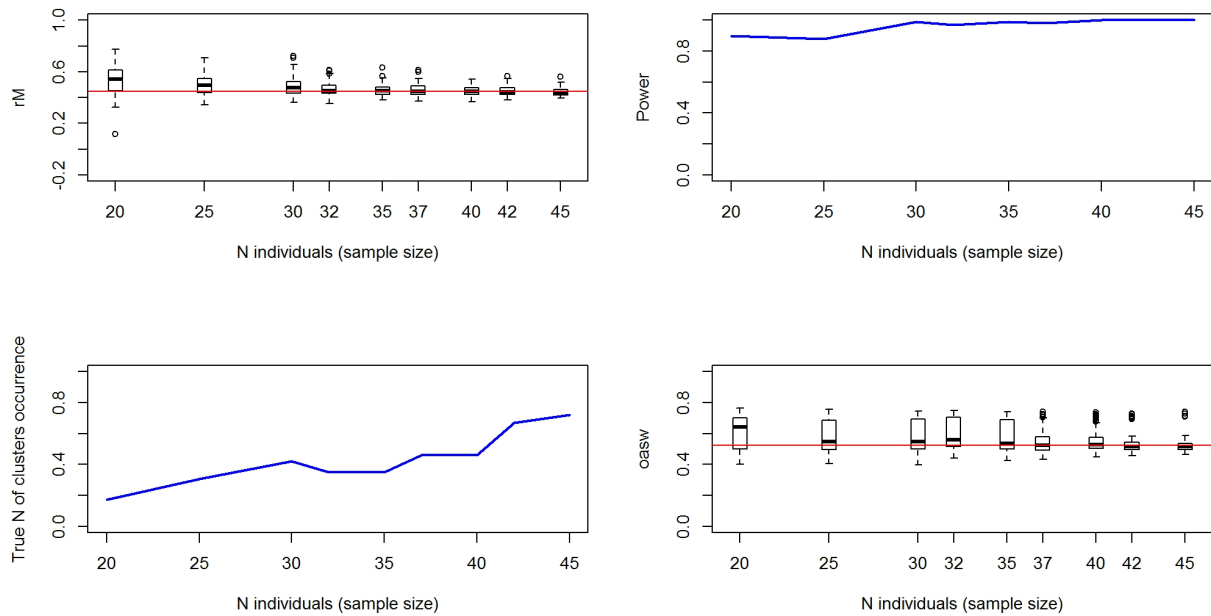


**Figure 04700-3.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.
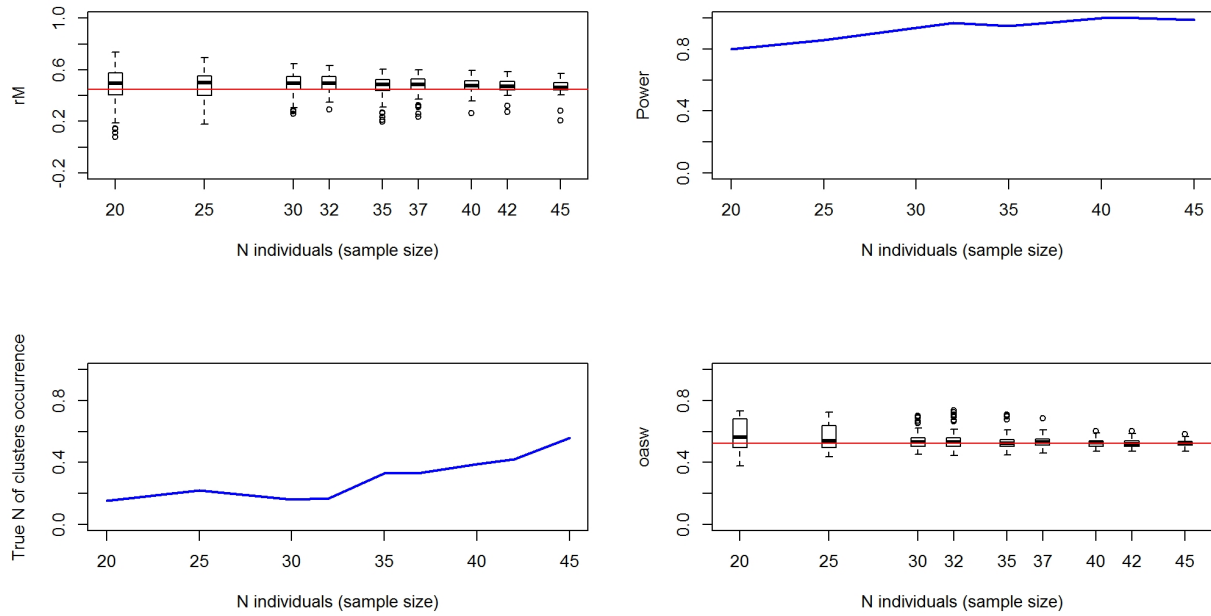


**Figure 04700-4.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

The comparison between the bootstrapped distribution of $r_M$ values from live recaptures and dead recoveries is not significant (p = 0.189); Figure 04700-5).
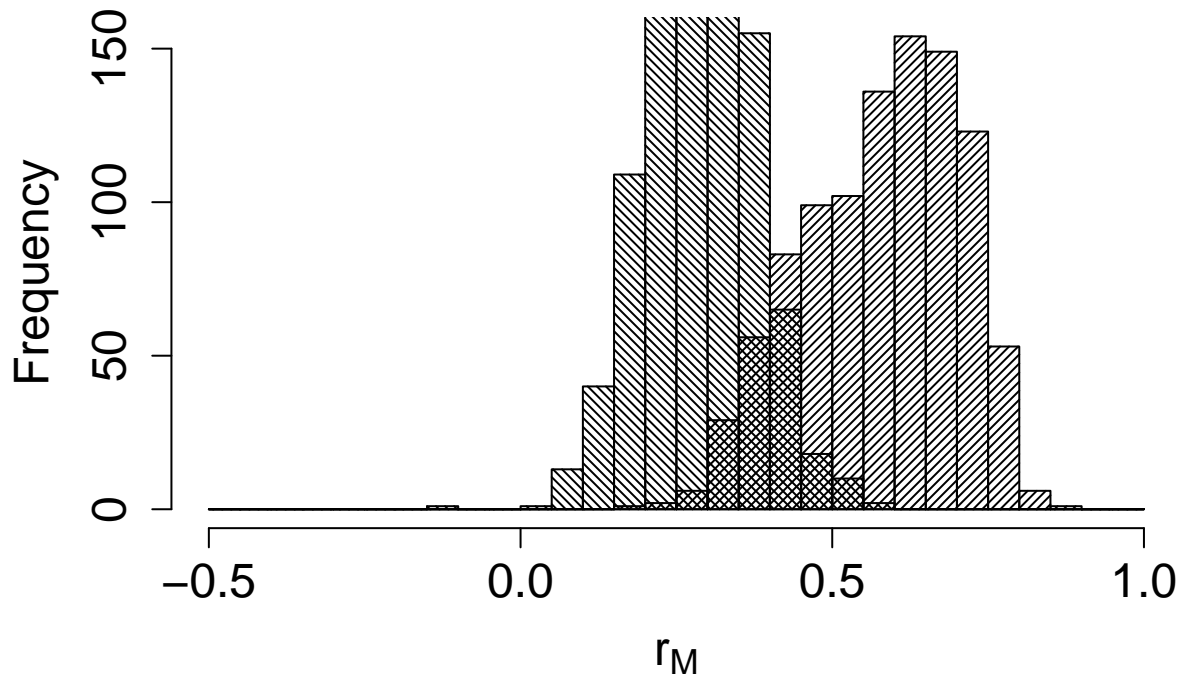
**Figure 04700-5.** Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

## 2. Connectivity between pre-defined regions

The species shows moderate/high connectivity (MC = 0.684; MC = 0.68 when adjusted for absolute abundance) between 5 breeding regions and 6 non breeding regions (Table 04700-2; Figure 04700-6).

**Table 04700-2.** Transition probabilities between pre-defined regions. Estimated abundance (number of individuals) in each breeding region is also reported.

| Breeding region | Abundance | Non breeding region | Transition probability |
|---|---|---|---|
| Central Europe | 2600 | North Africa | 0.053 |
| Central Europe | 2600 | North-west Europe | 0.158 |
| Central Europe | 2600 | South-west Europe | 0.105 |
| Central Europe | 2600 | West Europe | 0.684 |
| East Europe | 78579 | North Africa | 1.000 |
| North Europe | 67730 | North Africa | 0.119 |
| North Europe | 67730 | North-west Europe | 0.119 |
| North Europe | 67730 | South-central Europe | 0.024 |
| North Europe | 67730 | South-west Europe | 0.429 |
| North Europe | 67730 | West Africa | 0.071 |
| North Europe | 67730 | West Europe | 0.238 |
| North-west Europe | 112990 | North-west Europe | 1.000 |
| West Europe | 1216 | North-west Europe | 0.143 |

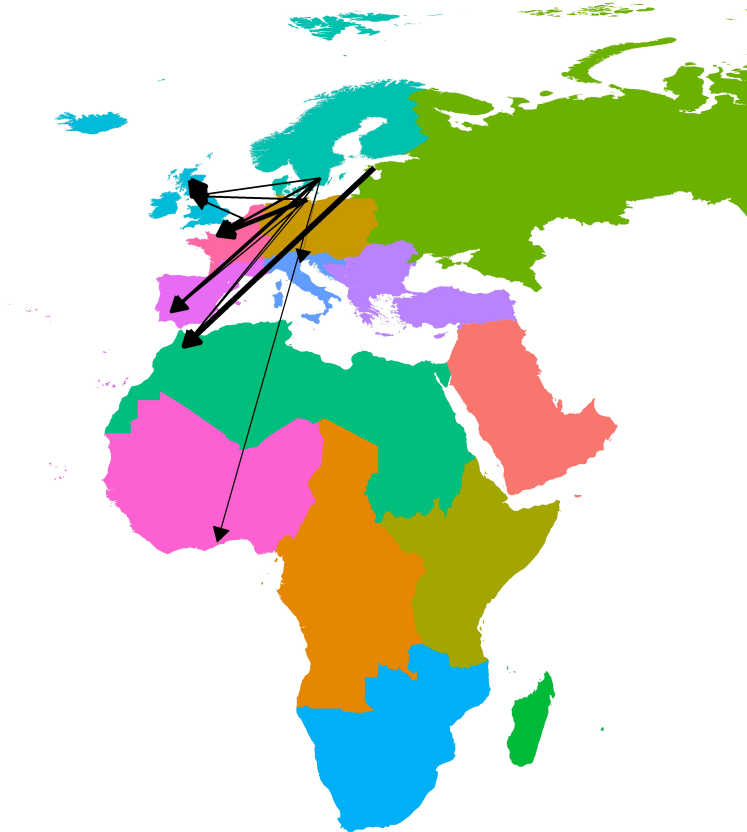| Breeding region | Abundance | Non breeding region | Transition probability |
|---|---|---|---|
| West Europe | 1216 | West Europe | 0.857 |



**Figure 04700-6.** Map showing pre-defined regions in different colours, with black arrows linking centroids of individual encounters in different regions. Arrow width is proportional to transition probability.

## Reference

BirdLife International and Handbook of the Birds of the World (2019). Bird species distribution maps of the world. Version 2019.1. Available at http://datazone.birdlife.org/species/requestdis.